DEX-0075

0500

RAW SEQUENCE LISTING
ERROR REPORT

Docket System ____✓____
Status Report ____✓____
Docket Book ____✓____

BIOTECHNOLOGY
SYSTEMS
BRANCH

SEP 2 1 2000

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/618,596_

9-13-2000
10-13-2000
(MAX) 3-13-2001

Source: _OIPE_

Date Processed by STIC: _7/28/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

aw Sequence Listing Erro   ummary

ERROR DETECTED SUGGESTED CORRECTION	SERIAL NUMBER: 09/618,596

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are ...ssing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING   DATE: 07/28/2000
PATENT APPLICATION: US/09/618,596   TIME: 14:55:17

Input Set : A:\Dex-0075.app
Output Set: N:\CRF3\07282000\I618596.raw

Does Not Comply
Corrected Diskette Needed

```
     3 <110> APPLICANT: Macina, Roberto A.
     4        Sun, Yongming
     6 <120> TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring, Staging,
     7        Imaging and Treating Colon Cancer
     9 <130> FILE REFERENCE: DEX-0075
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/618,596
C--> 12 <141> CURRENT FILING DATE: 2000-07-17
    14 <150> PRIOR APPLICATION NUMBER: 60/086,266
    15 <151> PRIOR FILING DATE: 1998-05-21
    17 <150> PRIOR APPLICATION NUMBER: PCT/US99/10498
    18 <151> PRIOR FILING DATE: 1999-05-12
    20 <160> NUMBER OF SEQ ID NOS: 1
    22 <170> SOFTWARE: PatentIn Ver. 2.0
    24 <210> SEQ ID NO: 1
    25 <211> LENGTH: 2608
    26 <212> TYPE: DNA
    27 <213> ORGANISM: Homo sapiens
    29 <400> SEQUENCE: 1
    30 gctgatagca cagttctgtc cagagaagga aggcggaata aacttattca ttcccaggaa 60
    31 ctcttggggt aggtgtgtgt ttttcacatc ttaaaggctc acagaccctg cgctggacaa 120
    32 atgttccatt cctgaaggac ctctccagaa tccggattgc tgaatcttcc ctgttgccta 180
    33 gaagggctcc aaaccacctc ttgacaatgg gaaactgggt ggttaaccac tggttttcag 240
    34 ttttgtttct ggttgtttgg ttagggctga atgtttcct gtttgtggat gccttcctga 300
    35 aatatgagaa ggccgacaaa tactactaca caagaaaaat ccttgggtca acattggcct 360
    36 gtgcccgagc gtctgctctc tgcttgaatt ttaacagcac gctgatcctg cttcctgtgt 420
    37 gtcgcaatct gctgtccttc ctgaggggca cctgctcatt ttgcagccgc acactgagaa 480
    38 agcaattgga tcacaacctc accttccaca agctggtggc ctatatgatc tgcctacata 540
    39 cagctattca catcattgca cacctgttta actttgactg ctatagcaga agccgacagg 600
    40 ccacagatgg ctcccttgcc tccattctct ccagcctatc tcatgatgag aaaagggggg 660
    41 gttcttggct aaatcccatc cagtcccgaa acacgacagt ggagtatgtg acattcacca 720
    42 gcgttgctgg tctcactgga gtgatcatga caatagcctt gattctcatg gtaacttcag 780
    43 ctactgagtt catccggagg agttattttg aagtcttctg gtatactcac caccttttta 840
    44 tcttctatat ccttggctta gggattcacg gcattggtgg aattgtccgg ggtcaaacag 900
    45 aggagagcat gaatgagagt catcctcgca agtgtgcaga gtctttgag atgtgggatg 960
    46 atcgtgactc ccactgtagg cgccctaagt ttgaaggca tccccctgag tcttggaagt 1020
    47 ggatccttgc accggtcatt ctttatatct gtgaaaggat cctccggttt taccgctccc 1080
    48 agcagaaggt tgtgattacc aaggttgtta tgcaccatc caaagttttg gaattgcaga 1140
    49 tgaacaagcg tggcttcagc atggaagtgg ggcagtatat ctttgttaat tgcccctcaa 1200
    50 tctctctcct ggaatggcat ccttttactt tgacctctgc tccagaggaa gatttcttct 1260
    51 ccattcatat ccgagcagca gggactgga cagaaaatct cataagggct ttcgaacaac 1320
    52 aatattcacc aattcccagg attgaagtgg atggtccctt ggcacagcc agtgaggatg 1380
    53 ttttccagta tgaagtgct gtgctggttg gagcaggaat tggggtcacc ccctttgctt 1440
    54 ctatcttgaa atccatctgg tacaaattcc agtgtgcaga ccacaacctc aaaacaaaaa 1500
    55 agatctattt ctactggatc tgcagggaga caggtgcctt ttcctggttc aacaacctgt 1560
    56 tgacttccct ggaacaggag atggaggaat taggcaaagt gggttttcta aactaccgtc 1620
    57 tcttcctcac cggatgggac agcaatattg ttggtcatgc agcattaaac tttgacaagg 1680
    58 ccactgacat cgtgacaggt ctgaaacaga aaacctcctt tgggagacca atgtgggaca 1740
```

```
         RAW SEQUENCE LISTING              DATE: 07/28/2000
         PATENT APPLICATION:  US/09/618,596    TIME: 14:55:17

         Input Set : A:\Dex-0075.app
         Output Set: N:\CRF3\07282000\I618596.raw

      59 atgagttttc tacaatagct acctcccacc ccaagtctgt agtgggagtt ttcttatgtg 1800
      60 gccctcggac tttggcaaag agcctgcgca aatgctgtca ccgatattcc agtctggatc 1860
      61 ctagaaaggt tcaattctac ttcaacaaag aaaatttttg agttatagga ataaggacgg 1920
      62 taatctgcat tttgtctctt tgtatcttca gtaattgagt ataggaata aggacggtaa 1980
W--> 63 tctgcatttt gtctctttgt atcttcagta atttacttgg tctattcagg tttgattagt 2040
      64 cactttagat aagaatgtgc ctctcaagcc ttgactccct ggtattcttt ttttgattgc 2100
      65 attcaacttc gttacttgag cttcagcaac ttaagaactt ctgaagttct taaagttctg 2160
W--> 66 aanttcttaa agcccatgga tcctttctca gaaaaataac tgtaaatctt tctggacagc 2220
W--> 67 catgactgta gcaaggcttg atagcagaag tttggtggtt canaattata caactaatcc 2280
      68 caggtgattt tatcaattcc agtgttacca tctcctgagt tttggtttgt aatcttttgt 2340
      69 ccctcccacc cccacagaag attttaagta gggtgacttt ttaaataaaa atttattgaa 2400
      70 taattaatga taaaacataa taataaacat aaataataaa caaaattacc gagaacccca 2460
      71 tccccatata acaccaacag tgtacatgtt tactgtcact tttgatatgg tttatccagt 2520
      72 gtgaacagca atttattatt tttgctcatc aaaaaataaa ggattttttt tcacttgaaa 2580
      73 aaaaaaaaaa aaaaaaaaaa aaaaaaaa                                     2608
```

see item 10 on
Err Summary
> item 10 Sheet

VERIFICATION SUMMARY   DATE: 07/28/2000
PATENT APPLICATION: US/09/618,596   TIME: 14:55:18

Input Set : A:\Dex-0075.app
Output Set: N:\CRF3\07282000\I618596.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:63 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:63 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:63 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:66 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:66 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:66 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:66 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:67 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:67 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:67 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:67 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1